REMARKS

Claims 1, 2, 5-18 and 22-45 are pending in the present Application. In the aforementioned Office Action, all of the claims were rejected as being unpatentable under §103 over Zenhausern (U.S. Patent Application Publication No. US2002/0094531) taken alone and over Chang (U.S. Patent No. 4,507,555) and Demirev (Analytical Chemistry, Vol. 69, No. 15, pp. 2893-2900) in view of Chalmers et al., Zeng et al., Zenhausern, Henry et al., Cotter et al., and Orient et al. Applicant requests consideration of these rejections in view of the arguments set forth below.

Rejections Based on Zenhausern

In advancing the aforementioned §103 rejections based on Zenhausern, the Examiner relies on Zenhausern as teaching an array of N sensing probes for use in analyzing biomolecules within a medium. The Examiner notes that Zenhausern discloses that each probe may take the form of a mass spectrometer, per paragraphs 0047, 0059 and 0069. The Examiner states that Zenhausern fails to teach submitting samples to a separation technique, but that doing so would be obvious to one of ordinary skill in the art.

Applicant submits that the Examiner has not given due consideration to all of the claim limitations, and thus has not established a prima facie case of unpatentability based on Zenhausern. Each of the independent claims recites limitations of analyzing multiple samples containing multiple proteins (derived from separation of samples obtained at multiple time intervals) by allocating the multiple samples among the mass spectrometry systems of a parallel array of mass spectrometry systems, such that each mass spectrometry system analyzes a different one of the protein samples. As is discussed in the present Application, this parallel processing technique enables proteomic studies to be performed in a time-effective manner. In contradistinction, Zenhausern does not teach that its sensing probe array can be used to conduct parallel analysis of multiple samples. Rather, as best as can be understood by Applicant (given that the Zenhausern disclosure is somewhat unclear with respect to the operation of its sensor

array), each sensing probe of the array is configured to sense a different molecule or combination of molecules within a single sample or, alternatively, to sense molecules or combinations of molecules at different locations within a single sample. See, e.g., paragraphs 0054, 0056 and 0058. Nowhere in Zenhausern is it taught or suggested that a sensor array may be beneficially utilized for parallel processing of multiple samples, as required by the independent claims.

More particularly, Zenhausern does not teach or suggest at least two claim limitations recited in each of the independent claims: (i) allocating multiple protein samples among mass spectrometry systems in an array, and (ii) each mass spectrometry system analyzing a different one of the multiple samples. With respect to (i), there is no need in Zenhausern to allocate (i.e., distribute in accordance with a prescribed method) multiple protein samples among mass spectrometry systems in an array, because Zenhausern describes analyzing only a single sample. With respect to (ii), each sensing probe of the Zenhausern array (assuming, arguendo, an equivalence between the claimed mass spectrometry systems and the sensing probes) does not analyze a different one of the multiple samples, but instead analyzes a different molecule of or location within a single sample.

Since Zenhausern does not teach or suggest all of the limitations present in the independent claims of the present Application, Applicant submits that the §103 rejection is improper and should be withdrawn. Applicant further submits that all of the dependent claims are patentable over Zenhausern for at least the reasons discussed above in connection with the independent claims from which they depend.

Rejections Based on Chang and Demirev

As noted above, all of the claims of the present Application were also rejected under §103 as being unpatentable over Chang (U.S. Patent No. 4,507,555) and Demirev et al. (Anal. Chem., Vol. 69, No. 15, pp. 2893-2900 (1997)) in view of Chalmers et al., Zeng et al., Zenhausern, Henry et al. (Anal. Chem. News and Features: Focus, April 1, 1999, p. 264A-268A), Cotter et al. (J. Mass Spectrometry, Vol. 34, pp.1368-1372 (1999)) and Orient et al. (Rev. Scientific Instruments, March 1997, Vol. 68, No. 3, pp. 1393-1397)). Applicant respectfully traverses these rejections.

Applicant has argued on multiple prior occasions during prosecution of the present Application that neither of the primary references on which the Examiner relies (Chang and Demirev et al.) teaches or suggests the claimed method or apparatus utilizing parallel analysis of multiple samples at individual mass spectrometry systems of an interconnected array. Instead, Chang teaches the use of two mass analyzers operating in different modes and arranged in parallel for simultaneously monitoring ions derived from a single sample, and Demirev et al. teaches a set of statistics that can be utilized to characterize the diversity in a combinatorial library of peptides. The Examiner admits at page 5 of the Office Action that "[t]he primary references...do not teach multiple system[s] of parallel mass-spectrometers that analyze the separated protein samples."

However, the Examiner proceeds to argue (at page 6) that "it would be prima facie obvious to analyze multiple protein samples using multiple mass-spectrometers instead of a single mass-spectrometers [sic], because prior art teaches processing of multiple samples using an array of equivalent devices, such as mass spectrometers (Zenhausern), and also teaches availability of simplified mass spectrometers better suited for combining into such multiple analyzing array." Applicant believes that this argument is based on a mischaracterization of the teachings of Zenhausern. As discussed above, Zenhausern does not teach processing of multiple samples using an array of equivalent devices, but instead teaches the use of an array of sensor probes to analyze a single sample, wherein each individual probe monitors a different molecular component of or location within a single sample. Neither Zenhausern nor the primary references suggest the desirability of combining individual mass spectrometer systems into an array such that multiple samples may be analyzed in parallel, nor do these references teach one of ordinary skill how one would implement such a parallel system, including the allocation and data collection functions thereof.

Furthermore, the teaching of providing miniaturized or otherwise simplified mass spectrometer designs, per the Henry et al., Cotter et al., and Orient et al. references, does not suggest to one of ordinary skill (either considered on their own or in combination with the other references) to combine such mass spectrometers in an interconnected parallel array, to allocate multiple protein samples among the individual mass spectrometers of the array, to analyze each sample at a different mass spectrometer, and to collect the resultant mass spectral data at a

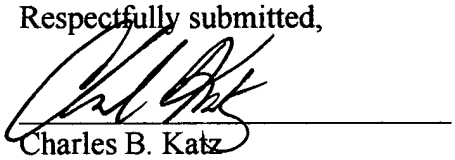
central computing resource, as is presently claimed. In the absence of such a suggestion, the Examiner is engaging in impermissible hindsight reconstruction of the claimed invention.

In sum, since none of the references, either taken alone or in combination, teach or suggest all of the limitations present in the independent claims of the present Application, Applicant submits that the §103 rejection is improper and should be withdrawn. Applicant further submits that all of the dependent claims are patentable over these references for at least the reasons discussed above in connection with the independent claims from which they depend.

In view of the arguments set forth above, Applicant believes that the claims are now in condition for allowance, and passage of the Application to issue is requested. If the Examiner believes that a telephone conference may be useful to advance the prosecution of the Application, he is invited to contact the Applicant's undersigned representative.

Dated: 28 February 2006

Respectfully submitted,

By: 

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